WHAT IS CLAIMED IS:

1. A predefined pooled collection of distinct nucleic acid vectors, wherein each constituent member of said pooled collection comprises an expression cassette that corresponds to a chromosomal transcript of known sequence.

2. The pooled collection according to Claim 1, wherein said collection comprises at least 100 distinct nucleic acid vectors.

3. The pooled collection according to Claim 2, wherein said collection comprises at least 1000 distinct nucleic acid vectors.

4. The pooled collection according to Claim 1, wherein said pooled collection is a library of ESTs.

5. A method of reducing expression of one or more chromosomal coding regions in a population of cells, said method comprising contacting said population of cells with a pooled collection of vectors according to Claim 1.

6. The method according to Claim 5, wherein said method is a method of identifying a genomic coding sequence of interest.

7. The method according to Claim 5, wherein said method is a method of determining function of a genomic coding sequence.

8. The method according to Claim 5, wherein said collection comprises at least 100 distinct nucleic acid vectors.

9. The method according to Claim 8, wherein said collection comprises at least 1000 distinct nucleic acid vectors.

10. The method according to Claim 5, wherein said pooled collection is a library of ESTs.

11. A method of identifying a genomic coding sequence of interest said method comprising:

(a) producing a non-cellular nucleic acid library by:

(i) dividing an initial set of a plurality of separate nucleic acids into two or more pooled collections having an initial sequence representation profile, wherein each pooled collection includes not more than about 100 distinct nucleic acids;

(ii) amplifying each of said pooled collections to produce two or more amplified pooled collections; and

(iii) combining said two or more amplified pooled collections to produce said non-cellular nucleic acid library, wherein said non-cellular nucleic acid library has a nucleic acid sequence representation profile that is substantially the same as said initial sequence representation profile;

(b) transforming a population of cells with said nucleic acid library to produce a cellular library; and

(c) identifying members of said cellular library that display a phenotype of interest to identify said genomic coding sequence of interest.

12. The method according to Claim 11, wherein said non-cellular nucleic acid library is an EST library.

13. The method according to Claim 11, wherein said non-cellular nucleic acid library is a library containing sequences complementary to at least a segment of a chromosomal transcript of a chromosomal transcript .

14. The method according to Claim 13, wherein said phenotype of interest results from loss of function of said genomic coding sequence of interest.

15. The method according to Claim 11, wherein said non-cellular nucleic acid library is a sense library.

16. The method according to Claim 11, wherein said non-cellular nucleic acid library is present in a vector system.

17. The method according to Claim 16, wherein said vector system is an integrating vector system.

18. The method according to Claim 11, wherein said non-cellular nucleic acid library comprises a substantially equal amount of each constituent nucleic acid member.

19. The method according to Claim 11, wherein said non-cellular nucleic acid library has a ratio of number of distinct nucleic acids to total amount of nucleic acid that ranges from about 10/μg to about 10,000/μg.

20. The method according to Claim 19, wherein said non-cellular nucleic acid library comprises at least about 1000 distinct nucleic acids of different sequence.

21. A method of identifying a genomic coding sequence of interest, said method comprising:

(a) producing a non-cellular expressed sequence tag (EST) library by:

(i) dividing an initial set of a plurality of separate ESTs into two or more pooled collections of ESTs having an initial EST representation profile, wherein each pooled collection includes not more than about 100 distinct ESTs;

(ii) amplifying each of said pooled collections to produce two or more amplified pooled collections; and

(iii) combining said two or more amplified pooled collections to produce said non-cellular EST library, wherein said non-cellular EST library has an EST representation profile that is substantially the same as said initial EST representation profile;

(b) transforming a population of cells with said non-cellular EST library to produce an EST cellular library; and

(c) identifying cellular members of said cellular library that display a phenotype of interest to identify said genomic coding sequence of interest,

wherein said phenotype of interest results from loss of function of said genomic coding sequence of interest.

22. The method according to Claim 21, wherein said non-cellular EST library is present in a vector system.

23. The method according to Claim 22, wherein said vector system is an integrating vector system.

24. The method according to Claim 21, wherein said non-cellular EST library comprises a substantially equal amount of each constituent EST member.

25. The method according to Claim 21, wherein said non-cellular EST library has a ratio of number of distinct ESTs to total amount of nucleic acid that ranges from about 10/μg to about 10,000/μg.

26. The method according to Claim 25, wherein said non-cellular EST library comprises at least about 1000 distinct ESTs of different sequence.

27. A method of producing a non-cellular nucleic acid library, said method comprising:

(a) dividing an initial set of a plurality of separate nucleic acids into two or more pooled collections of nucleic acids having an initial sequence representation profile, wherein each pooled collection includes not more than about 100 distinct nucleic acids;

(b) amplifying each of said pooled collections to produce two or more amplified pooled collections; and

(c) combining said two or more amplified pooled collections to produce said non-cellular nucleic acid library, wherein said non-cellular nucleic acid library has a sequence representation profile that is substantially the same as said initial sequence representation profile.

28. The method according to Claim 27, wherein said non-cellular nucleic acid library is an EST library.

29. The method according to Claim 27, wherein said non-cellular nucleic acid library is a library containing sequences complementary to at least a segment of a chromosomal transcript of a chromosomal transcript.

30. The method according to Claim 27, wherein said non-cellular nucleic acid library is present in a vector system.

31. The method according to Claim 27, wherein said vector system is an integrating vector system.

32. The method according to Claim 27, wherein said non-cellular nucleic acid library comprises a substantially equal amount of each constituent nucleic acid member.

33. The method according to Claim 27, wherein said non-cellular nucleic acid library has a ratio of number of different nucleic acids to total amount of nucleic acid that ranges from about 10/μg to about 10,000/μg.

34. The method according to Claim 33, wherein said non-cellular nucleic acid library comprises at least about 1000 nucleic acids of different sequence.

35. A non-cellular nucleic acid library produced according to the method of Claim 27.

36. A cellular nucleic acid library produced by transforming a population of cells with a non-cellular library according to Claim 35.

37. A method of identifying a genomic coding sequence of interest, said method comprising:

(a) transforming a population of cells with a predefined pooled collection of distinct nucleic acid vectors, wherein each constituent member of said pooled collection comprises an expression cassette that corresponds to a chromosomal transcript of known sequence; and

(b) identifying members of said cellular library that display a phenotype of interest to identify said genomic coding sequence of interest.

38. A cellular member of said cellular library produced according to the method of Claim 37.

39. The cellular member according to Claim 38, wherein said cellular member displays a phenotype of interest that caused by inactivation of a genomic coding sequence by a nucleic acid vector member of said pooled collection.

40. A genomic coding sequence present in other than its natural environment identified according to the method of Claim 37.

41. A nucleic acid transcript of a genomic coding sequence according to Claim 40.

42. An expression product of a genomic coding sequence according to Claim 40.

43. A method of treating a subject suffering from an anthrax mediated disease condition, said method comprising:

administering to said subject an effective amount of ARAP3 inhibitory agent to treat said subject.

44. A method of confering an anthrax resistant phenotype on a subject, said method comprising:

administering to said subject an effective amount of an ARAP3 inhibitory agent.